IN THE SPECIFICATION

At page 11, line 21 please substitute the following paragraph:

The LPS from PGEM (31 mg), pGEMLOS-4 (25 mg), pGEMLOS-5 (15 mg), and pGEMLOS-7 (4.4 mg) was hydrolyzed in 1% acetic acid (2 mg LPS/ml) for 2 hours at 100° C. The hydrolysates were centrifuged at 5000 g for 20 min at 4° C. and the supernatants removed. The pellets were washed with 2 ml of H_2O and centrifuged again (5000 g, 20 min, 4° C). The supernatants and washings were pooled and lyophilized to give the oligosaccharide fractions. As a standard, 10 mg of LPS from Salmonella typhimurium TV 119 Ra mutant (~~Sigma~~ Sigma®, St. Louis) was treated in the same fashion.

At page 11, line 29 please substitute the following paragraph:

To prepare desalted oligosaccharide pools for ESI-MS analysis, small aliquots of the crude oligosaccharide fractions (<2 mg) were chromatographed on two Bio-Silect™ ~~Bio-Select~~ SEC 125-5 HPLC columns (Bio-Rad® ~~Bio-Rad~~, Richmond, Calif.) connected in series, using 0.05 M pyridinium acetate (pH 5.2) at a flow rate of 1 ml/min. A refractive index detector was used to monitor column effluent and chromatograms were recorded and stored with an integrator.

At page 12, line 5 please substitute the following paragraph:

For large scale separations, the oligosaccharide fractions from PGEM (10.2 mg), pGEMLOS-4 (9.3 mg), and pGEMLOS-5 (7.0 mg) were dissolved in 0.3 ml of 0.05 M pyridinium acetate buffer (pH 5.2) and centrifuge-filtered through a 0.45 gm Nylon-66 membrane. The PGEM and pGEMLOS-4 samples were applied to a single Bio-Gel® ~~Bio-Gel~~ P-4 column (1.6 x 84 cm, <400 mesh; Bio-Rad® ~~Bio-Rad~~), and the pGEMLOS-5 sample was applied to two Bio-Gel® ~~Bio-Gel~~ P-4 columns connected in series (1.6 x 79 cm and 1.6 x 76.5 cm). The columns were equipped with water jackets maintained at 30° C. Upward elution at a flow rate of 10 ml/h was achieved with a P-1 peristaltic pump (Pharmacia™ ~~Pharmacia~~, Piscataway). Effluent was monitored with refractive index and fractions were collected at 10 minute intervals and evaporated to dryness in a concentrator.

At page 12, line 18 please substitute the following paragraph:

Oligosaccharide fractions were placed in 1.5 ml polypropylene tubes and treated with cold 48% aqueous hydrogen fluoride to make 5-10 μg/ml solutions. Samples were kept for 18 hours at 4°C and then aqueous HF was evaporated. The dephosphorylated samples were then rechromatographed on two Bio-Silect™ ~~Bio-Select~~ SEC 125-5 HPLC columns connected in series using 0.05 M pyridinium acetate (pH 5.2).

At page 13, line 2 please substitute the following paragraph:

Dephosphorylated oligosaccharide fractions were dissolved in 400 μl of 2 M trifluoroacetic acid and heated for 4 hours at 100° C. The hydrolysates were evaporated to dryness in a SpeedVac® ~~Speed-Vac~~ concentrator, redissolved in 20 μl H_2O, and dried again. Hydrolysates were analyzed by high-performance anion exchange chromatography with pulsed amperometrie detection using a Dionex® BioLC® ~~Dionex BioLC~~ system (Dionex® ~~Dionex~~, Sunnyvale, Calif.) with a CarboPac™ ~~CarboPac~~ PA1 column.

At page 14, line 15 please substitute the following paragraph:

O-Deacylated LPS samples were analyzed on a Voyager™ ~~Voyager~~ or an Elite™ ~~Elite~~ MALDI-TOF instrument (PerSeptive™ ~~PerSeptive~~ Biosystems, Framingham, Mass.) equipped with a nitrogen laser (337 nM). All spectra were recorded in the negative-ion mode using delayed extraction conditions as described in detail elsewhere. (Gibson et al. J. Amer. Soc. Mass Spec. 8:645-658 (1997)). Samples were dissolved in H_2O (approx. 250 pmol/μl), and mixed 1:1 with the matrix solution (a saturated solution of 2,5-dihydroxybenzoic acid in acetone) and allowed to dry at room temperature on a gold-plated MALDI plate. Approximately 100 laser shots were recorded for each sample, averaged and then mass calibrated using an external mass calibrant consisting of renin substrate tetradecapeptide, insulin chain B, oxidized, and bovine insulin (all from ~~Sigma~~ Sigma®). For external calibrations under these conditions, a mass accuracy of 0.1% was obtained For comparison purposes, a single point correction was made to the spectra of the O-deacylated LPS from PGEM using the expected lipid A fragment ion ((M-H) average=952.009), and then the spectra for the three chimeric strains were recalibrated using this lipid A fragment ion and an additional ion from PGEM (m/z 2835.7) present in all four samples.